Figure 2: The polynucleotide sequence of apo-dystrophin-4. The inversion sequence shown in Figure 1 begins at base pair 860 and ends at base pair 996. The sixteen peptides coded for by the entire sequence are SEQ ID NOs: 38 through 50 and 35 through 37, respectively.

At page 3, line 26, please replace the entire paragraph beginning "Figure 6:" with the following paragraph:

Figure 6: The full-length apo-dystrophin-4 cDNA and upstream genomic sequence translated. Genomic sequence upstream of the apo-dystrophin-4 cDNA is shown from -233 to -1, the start of the apo-4 sequence. (SEQ ID NO: 51). The peptides coded for by the sequence are listed as SEQ ID NOs: 52, 53, 38-50 and 35-37, respectively. The sequence was subjected to a MacVector alignment and was homologous with the 3' end of the dystrophin cDNA, up until the inversion at 860. A search of the 3' 137 bp of apo-4 alone showed that it was precisely homologous to 3' dystrophin sequence 1.62 Kb downstream in the 3' UTR in the reverse orientation and was thus an inversion of the 3' UTR and genomic sequence. Three potential starting methionines are highlighted at +25, +88, and +100. and a potential CAAT box is underlined at +57. These M's are in phase I of apo-4 alone, but appear in phase II here due to the presence of upstream sequence. The longest open reading frame that should be obtainable from this sequence begins with the M at +88 (33aa). The beginning of exon 79 at 453 is also underlined. For a predicted protein in frame 2, a putative transmembrane domain is underlined and putative N-glycosylation sites that follow the Asn-Xxx-Ser/Thr motif are shown (in parentheses when utilized if nonsense suppression occurs). A cryptic polyadenylation site is underlined at +990. The upstream exon identified by GRAIL appears from -90 to -5.